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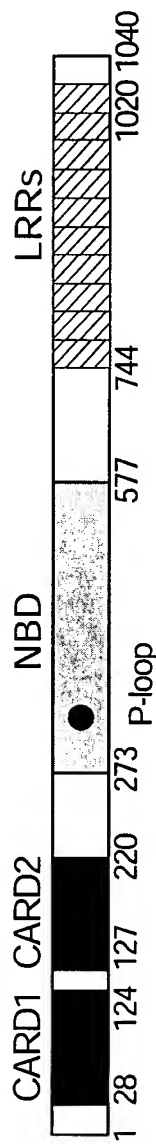


Figure 1

A

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Nod2(2)	127	SEHP-ARDLOSHPAVERIHSIV	--ENMELAMERGEVSQECDEELPHIT	PSQARRLDLDATVKAAGLAELLQVCE	EPVPLAIPLEAATCK		
Nod1	15	ESPHIQILKSNRELLVTHIRNTQ	---CLVDNLLKNDYFSDADAVACPTQ	PDKVRKLLDLVOSKEEVSFFLYLLQQ	LADAVDLISWILLE		
RICK	434	-GIAQNTQOSREDIVNCTEACL	---NOSDALLSDLLIMKEDYEVASTKPT	TSKVRQLDITDLOGEEFAKVIQKED	--NKOMGQVNPETLV		
ARC	6	-BEPSETHDRERKREVELQADSG	---LLHDAVARGVLTGPEYBALDALPA	ERRVRELLLVOSKGAACQELLRC	QOQTVSMFDPAMDWQVGP		
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Ced-4	2	LCIECEALSTHTRILHDFEPK	---DALTYLEGKRIFTEDHSELISKMS	ERERIANFLRYERQASSELGPIIDFEN	--NNQSHADAELEYI		
Caspase-9	1	MDADRRLRRCGRRLMEELND	---OLMDVLSSELEFEMIEDQKAGSGSRDQRLID	ETREGSCALPEISCLIED	--TGODMLASFLITNR		
Apaf-1	1	MDAKERNCALQHEALEXDKTS	---YIMDEMIISDCELTTHSEERKVRNEPTQ	---OQRAAMLIKMIILKONDSVVSYNALIH	EGKOLAALLHDCIPV		
C-IAP1	453	MASDDLSTHIRKEMALFOQLTCVL	---PIIDNLLKRNVINKOEFDIILKQKTC	---PCARELIDITVWVKGNAAPALFNCLKE	--PDSLTLYKQNFVDEN		

B

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Apaf-1	226	RSLLIDDDYMS	-----	WYLKAFDSQCOHITLIRKSKVTD	---SYNGPKYMPVRESSGKEKGL	ETLSLVN	---MKKADPEQSHSTRECKSPLV	
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Ced-4	331	ATLMMFKSCPEKTEKMAQL	-----	NNKLES	RGLVGEVCIITPYSKSLAMALQRC	VEVLSDEDRSLAF	VVMPPQ	VDIPVWKLNSCTIPVD

C

		α	β
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Repeat 3	800	NSVGDIGVEQLLPCL	---GVCKALYERD
Repeat 4	825	NNESDRGIYKLECALHCEQLQKALFN	
Repeat 5	853	NKQTDGCAHSMAKILLACRQNHALLRLGN	
Repeat 6	881	NYETAGAQVLAEGLRGNTSLQPLGANG	
Repeat 7	909	NNVGDGEQAQALAEALGDHQSRLWLSLVG	
Repeat 8	937	NNEGSVGAQALALMLAKNMVLEELCLSE	
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Repeat 10	993	NCELYLGAENLLQALERNDTLELVWVRG	

Figure 2

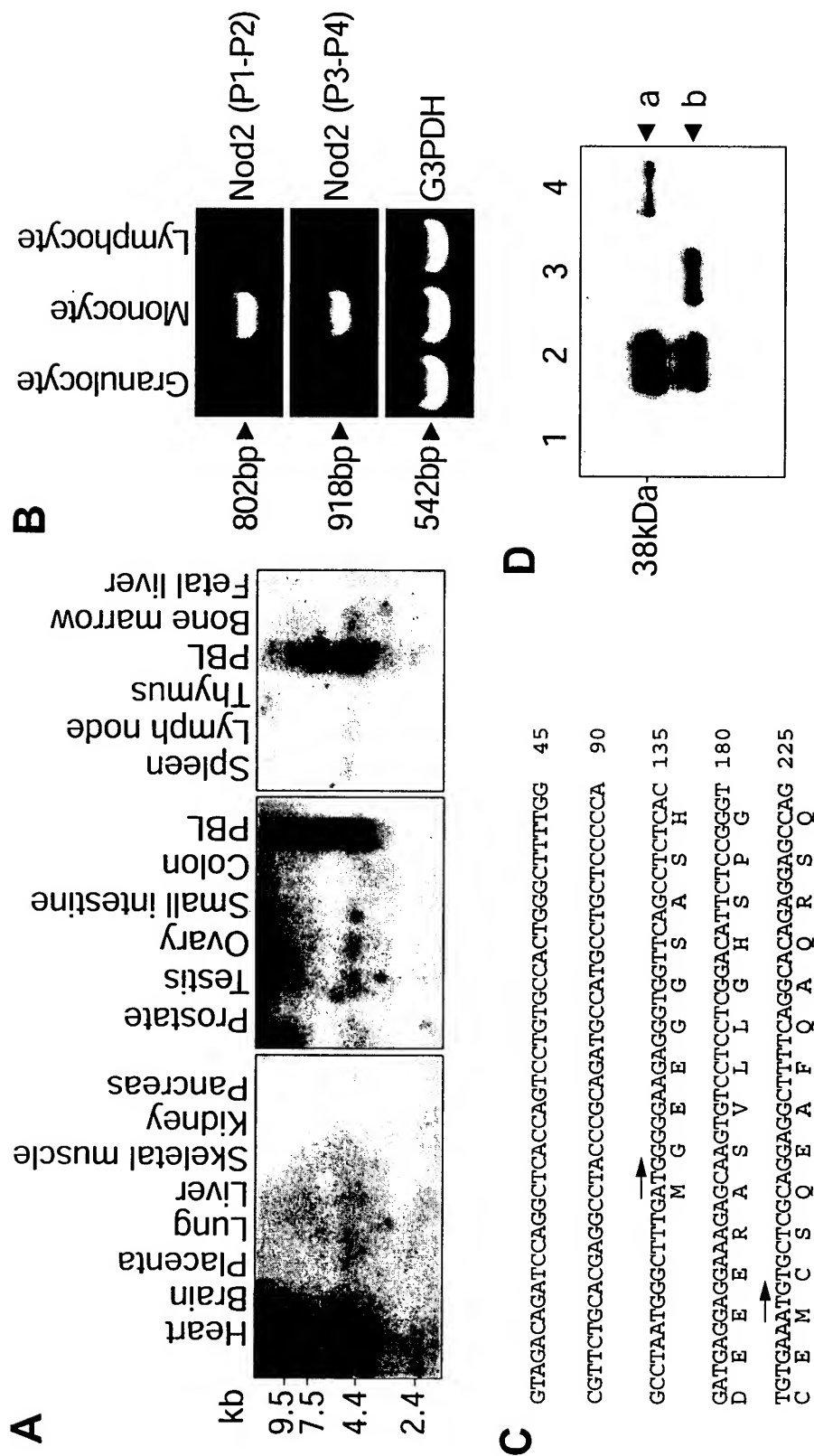


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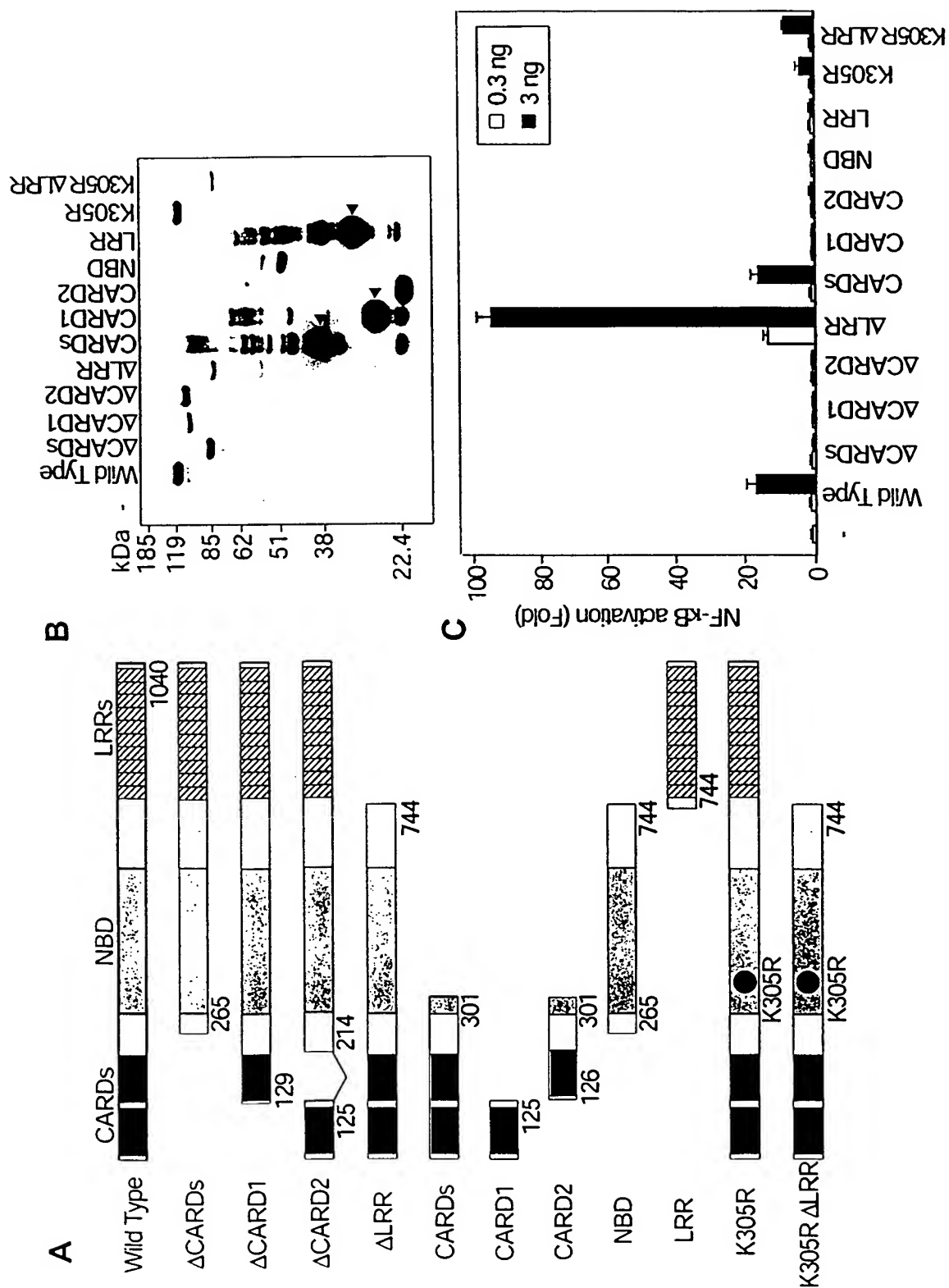


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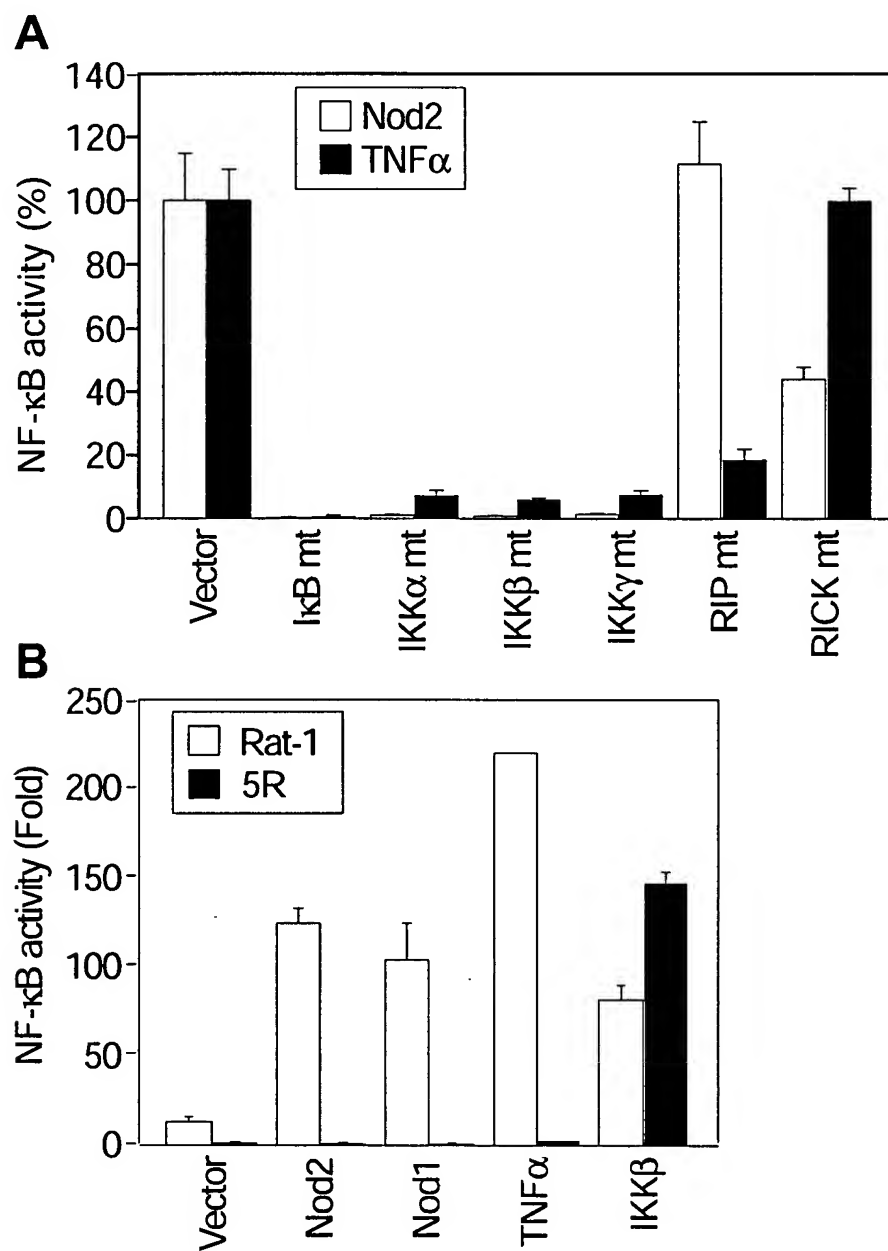


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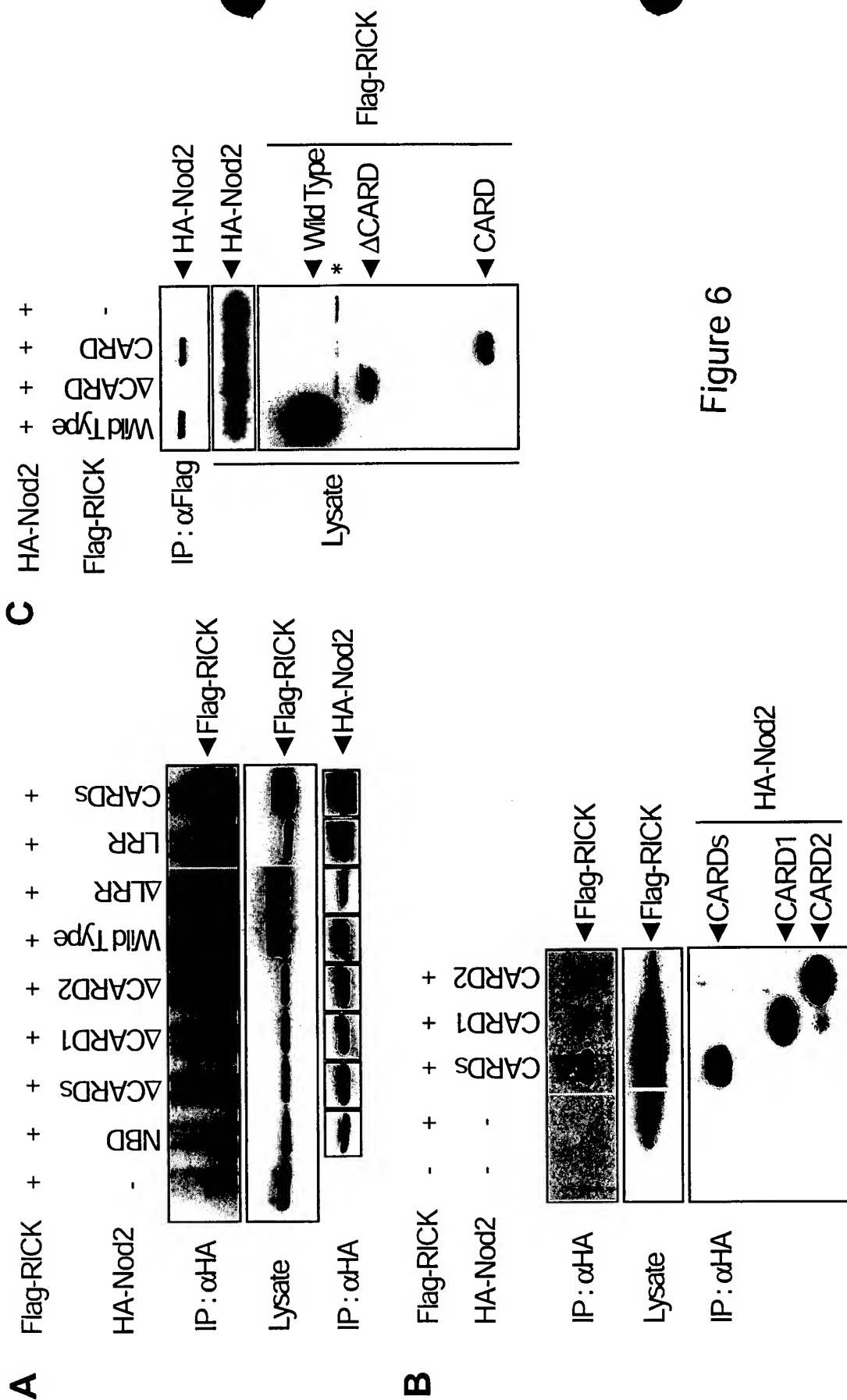


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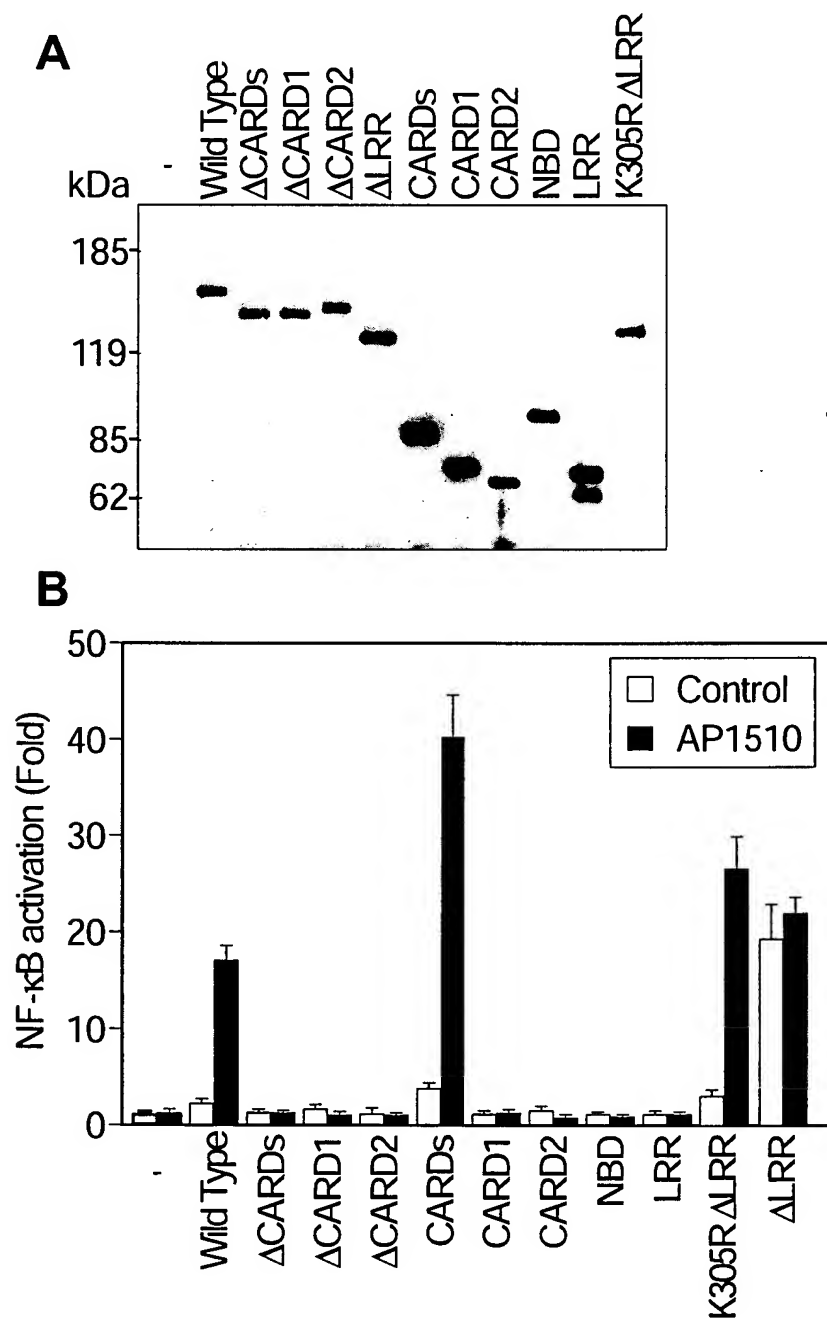


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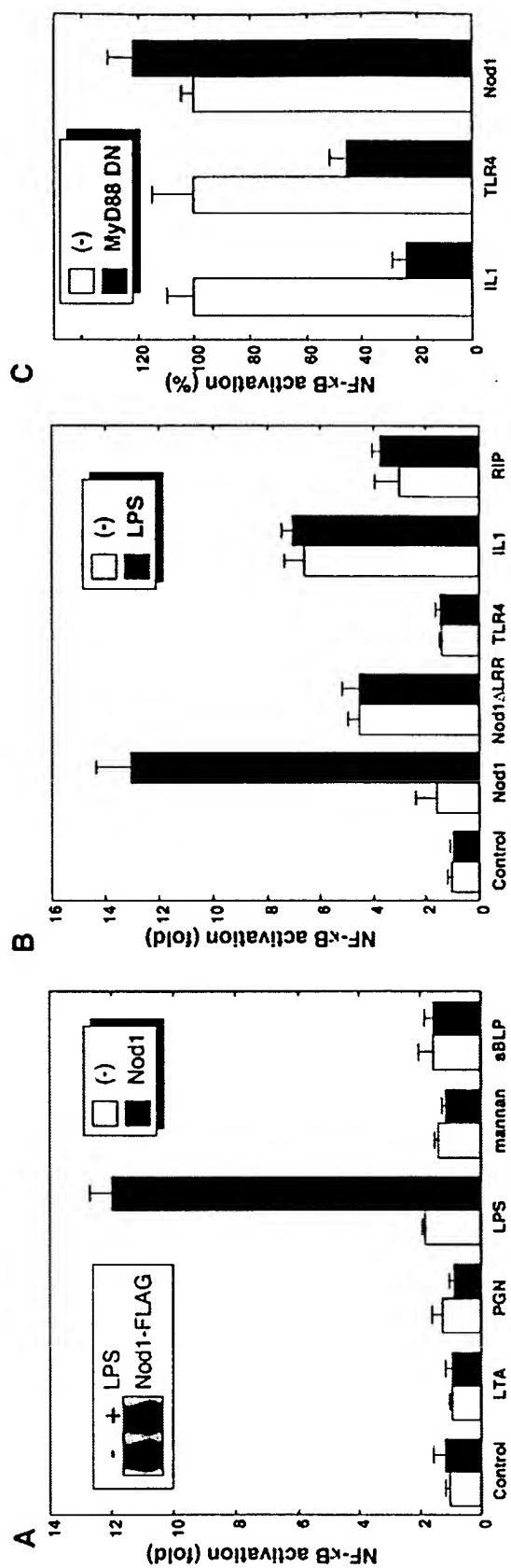


Figure 8

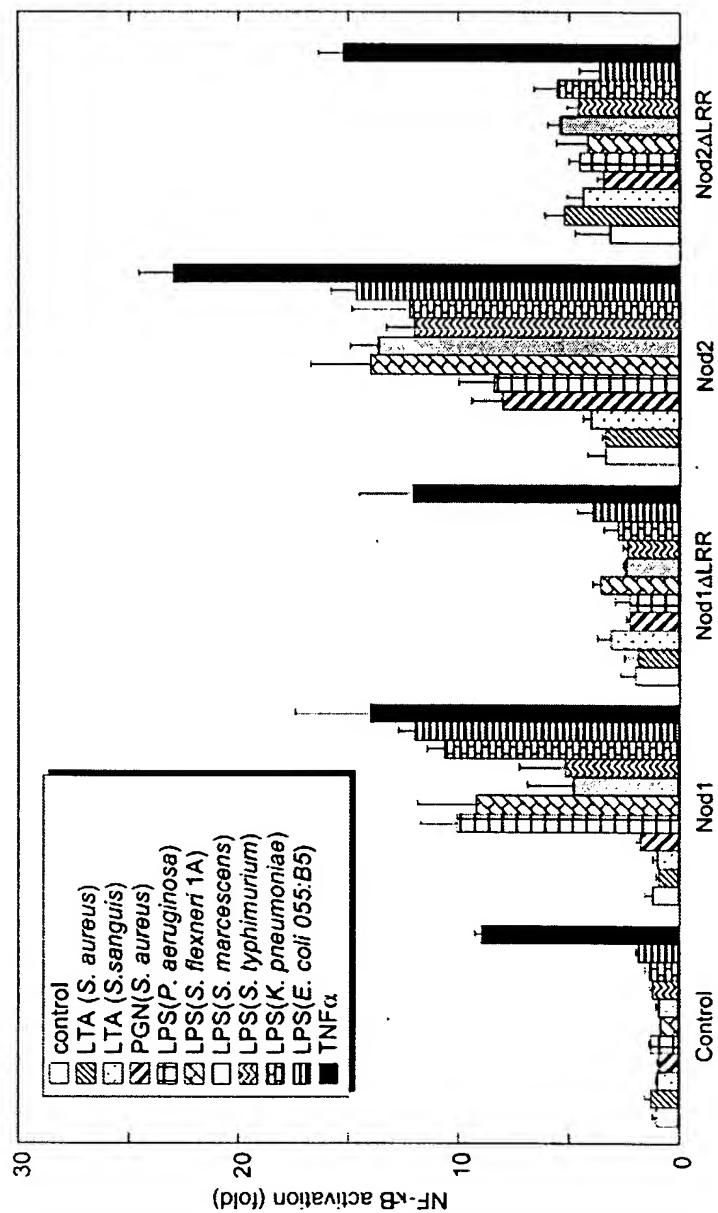


Figure 9

10002934-102601

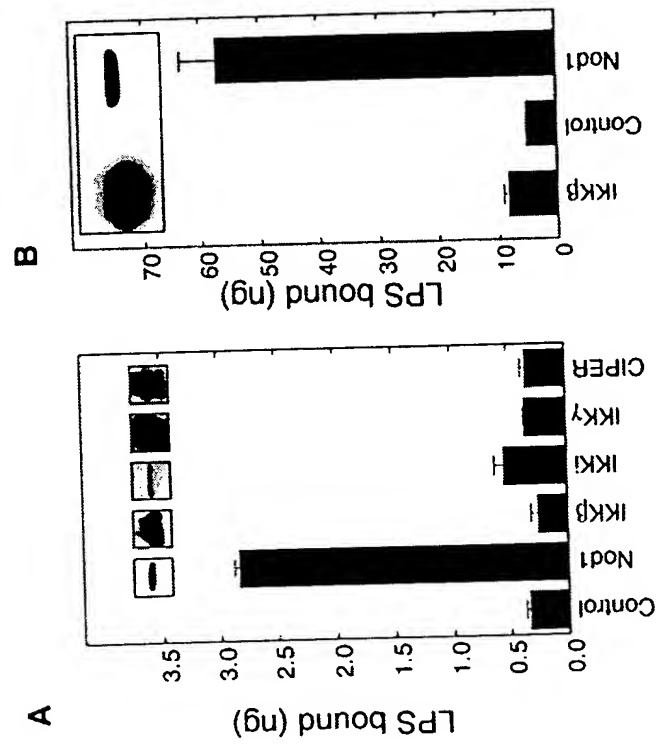


Figure 10

Figure 11

SEQ ID NO:33

Nod2 cDNA sequence

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Figure 13
SEQ ID NO:2

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RGRLPTLLHL GRLALWGLGM CCYVSAQQL QAAQVSPDDI SLGFLVRAKG VVPGSTAPLE
FLHITFCFF AAFYLALSAD VPPALLRHLEF NCGRPGNSPM ARLLPTMCIQ ASEGKDSSVA
ALLQKAEPHN LQITAAFLAG LLSREHWGLL AECQTSEKAL LRRQACARWC LARSLRKHFH
SIPPAAPGEA KSVHAMPFI WLIRSLYEMQ EERLARKAAR GLNVGHLKLT FCSVGPTCA
ALAFVLQHLR RPVALQLDYN SVGDIGVEQL LPCLGVCKAL YLRDNNISDR GICKLIECAL
HCEQLQKLAL FNNKLTGCA HSMAKLLACR QNFLALRLGN NYITAAGAQQV LAEGLRGNTS
LQFLGFWGNR VGDEGAQALA EALGDHQSLR WLSLVGNNIG SVGAQALALM LAKNVMLEEL
CLEENHLQDE GVCSLAEGLK KNSSLKILKL SNNCITYLGA EALLQALERN DTILEVWLRG
NTFSLEEVDK LGCRDTRLLL *

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Figure 14

SEQ ID NO:3

MCSQEAFQAA RSQVLELLVS GSLEGFESVL DWLLSWEVLS WEDYEGFHLL GQPLSHLARR
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HVENMLDLAW ERGFVSQYEC DEIRLPIFTP SQRARRLLDL ATVKANGLAA FLLQHVQELP
VPLALPLEAA TCKKYMALR TTVSAQSRFL STYDGAETLC LEDIYTENVL EVWADVGMAG
PPQKSPATLG LEELFSTPGH LNDDADTVLV VGEAGSGKST LLQRLHLLWA AGQDFQEFLF
VFPFSCRQLQ CMAKPLSVRT LLFEHCCWPD VGQEDIFQLL LDHPDRVLLT FDGFDEFKFR
FTDRERHCSP TDPTSVQTLL FNLLQGNLLK NARKVVTSRP AAVSAFLRKY IRTEFNKGF
SEQGIELYLR KRHHPEGVAD RLIRLLQETS ALHGLCHLPV FSWMVSKCHQ ELLQEGGSP
KTTTDMYLLI LQHFLHATP PDSASQGLGP SLLRGRLLPTL LHLGRLALWG LGMCCYVFA
QQLQAAQVSP DDISLGFLVR AKGVVPGSTA PLEFLHITFQ CFFAAFYAL SADVPPALLR
HLFNCGRPGN SPMARLLPTM CIQASEGKDS SVAALLQKAE PHNLQITAAF LAGLLSREHW
GLLAECQTSE KALLRRQACA RWCLARSLRK HFHSIPPAAP GEAKSVHAMP GFIWLIRSLY
EMQEERLARK AARGLNVGHL KLTFCVSGPT ECAALAFVLQ HLRRPVALQL DYNSVGDIGV
EQLLPCLGVC KALYLRDNNI SDRGICKLIE CALHCEQLQK LALFNNKLTG GCAHSMAKLL
ACRQNFALR LGNNYITAAG AQVLAEGLRG NTSLQFLGFW GNRVGDEGAQ ALAEALGDHQ
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LKLSNNCITY LGAEALLQAL ERNDTILEVW LRGNTFSLEE VDKLGCRDTR LLL*

10002974.102601

Figure 15
SEQ ID NO:34

Nod2a AA sequence, Mutant

MGEEGGSASH DEEERASVLL GHSPGCEMCS QEAFQAQRSQ LVELLVSGSL EGFESVLDWL
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GCWDPHSLHP ARDLQSHRPA IVRRLHSHVE NMLDLAWERG FVSQYECDEI RLPIFTSPQR
ARRLLDLATV KANGLAAFLQ QHVQELPVPL ALPLEAATCK KYMAKLRTTV SAQSRFLSTY
DGAETLCLED IYTENVLEWV ADVGMAGPPQ KSPATLGLEE LFSTPGHLND DADTVLVVGE
AGSGKSTLLQ RLHLLWAAGQ DFQEFLFVFP FSCRQLQCMK KPLSVRTLLF EHCCWPDVGO
EDIFQLLLDH PDRVLLTFDG FDEFKFRFTD RERHCSPTDP TSVQTLLEFN LQGNLLKNAR
KVVTSRPAAV SAFLRKYIRT EFNKGFSEQ GIELYLRKRH HEPGVADRLL RLLQETSALH
GLCHLPVFSW MVSCKHQELL LQEGGSPKTT TDMYLLILQH FLLHATPPDS ASQGLGPSLL
RGRLPTLLHL GRLALWGLGM CCYVFAQQQ QAAQVSPDDI SLGFLVRAKG VVPGSTAPLE
FLHITFQCFE AAFYLALSAD VPPALLRHLE NCGRPGNSPM ARLLPTMCIQ ASEGKDSSVA
ALLQKAEPHN LQITAAFLAG LLSREHWGLL AECQTSEKAL LRRQACARWC LARSLRKHFH
SIPPAAPGEA KSVHAMPGFI WLIRSLYEMQ EERLARKAAR GLNVGHLKLT FCSVGPTECA
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HCEQLQKLAL FNNKLTGCA HSMAKLLACR QNFLALRLGN NYITAAGAQQ LAEGLRGNTS
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10002974.102601

FIGURE 16

Nod2 Exon11, Wild type

cagacatgag caggatgtgt ctaagggaca ggtgggcttc agtagactgg ctaactcctg

cagtctcttt aactggacag tttcaagagg aaaaccaaga atccttgaag ctcaccattg

tatcttcttt tccagGTTGT CCAATAACTG CATCACCTAC CTAGGGGCAG AAGCCCTCCT

L S N N C I T Y L G A E A L L

GCAGGCCCTT GAAAGGAATG ACACCATCCT GGAAGTCTGg taaggcccct gggcaggcct

Q A L E R N D T I L E V

gttttagctc tccgaacctc agtttttcta tctgtaaaat ggggtgacgg gagagaggaa

tggcagaatt ttgaggatcc cttctgattc tgacattcag tgagaatgat tctgcatgtg

Nod2 Exon11, Mutant

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tatcttcttt tccagGTTGT CCAATAACTG CATCACCTAC CTAGGGGCAG AAGCCCTCCT

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10002974-102601

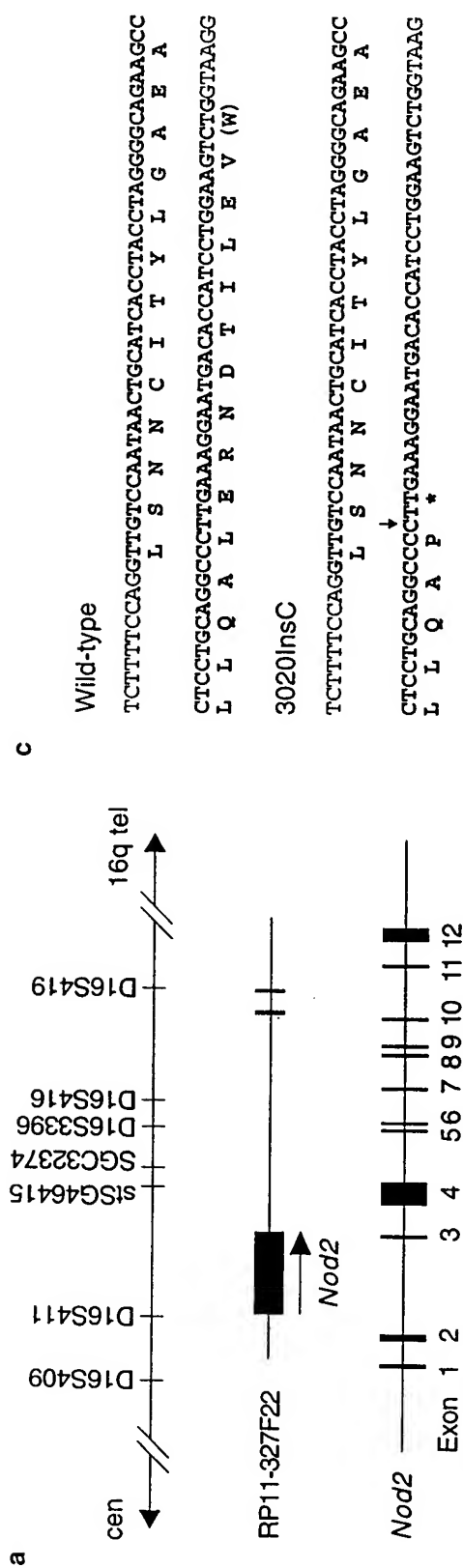
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g

10002974-102601



c

Wild-type

TCCTTCCAGGTTGTCCAAATGATGATCCTACCTAGGGGAGAAGCC
L S N N C I T Y L G A E A

CTCCTGCAGGCCCTTGAAGGAATGACACCATCTGGAAGTCTGGTAAGG
L L Q A L E R N D T I L E V (W)

3020InsC

TCCTTCCAGGTTGTCCAAATGATGATCCTACCTAGGGGAGAAGCC
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L L Q A P *

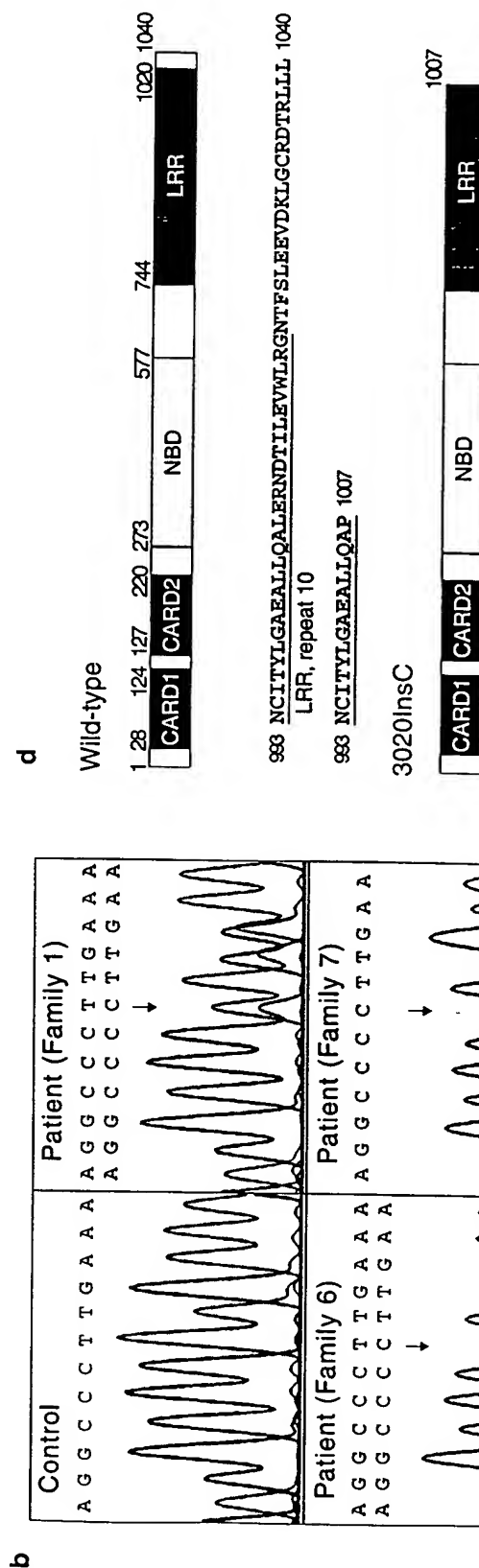


Figure 17

10002974-102601

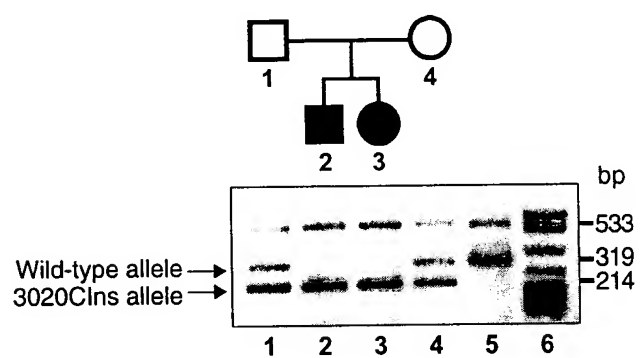


Figure 18

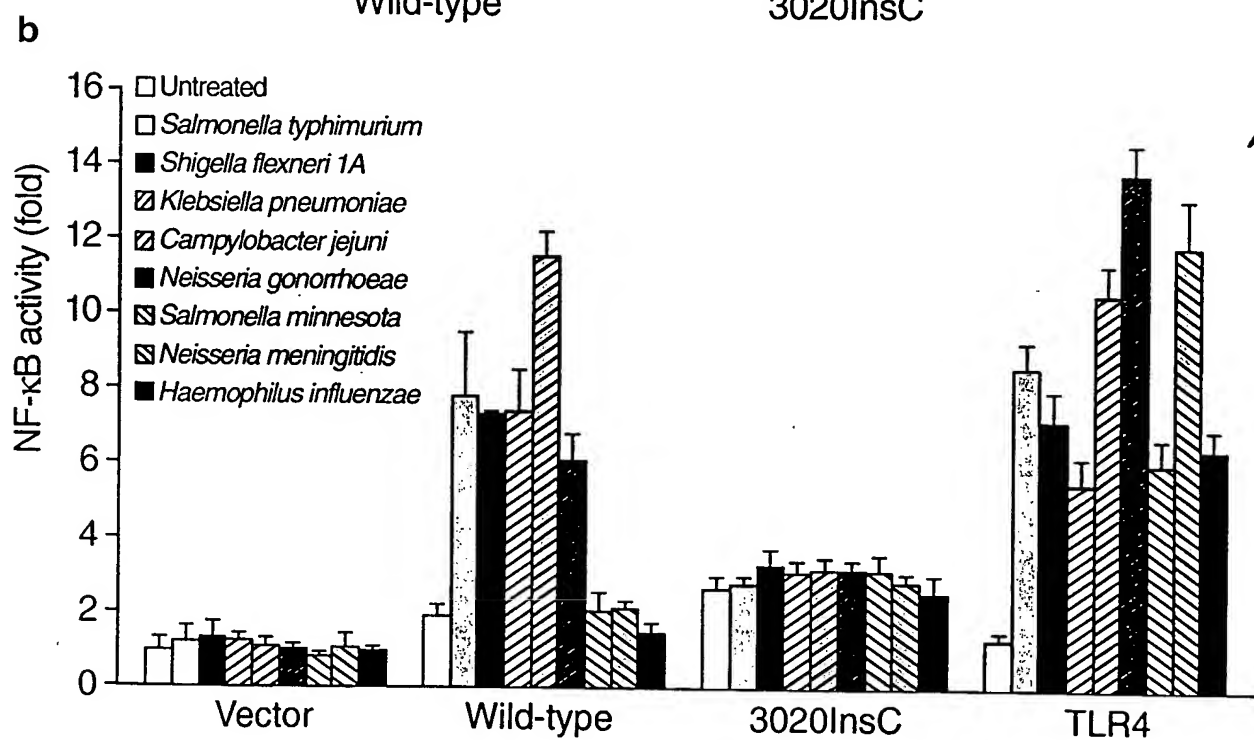
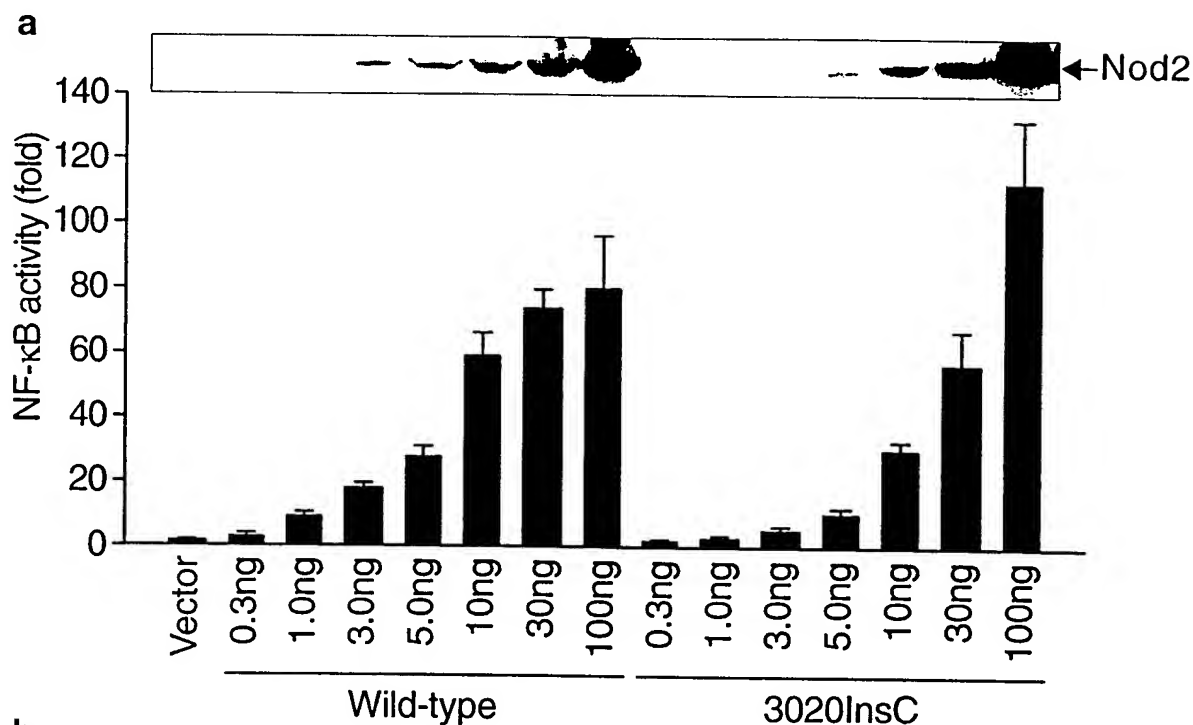


Figure 19

[illegible]

Figure 1

(a) **Flowchart illustrating the process of identifying potential confounders.**

(b) **Flowchart illustrating the process of selecting variables for multivariable analysis.**

Figure 21
SEQ ID NO: 54

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ttga

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THE UNIVERSITY OF CHICAGO

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180	GCWDPHSLHP	ARDLQSHRPA	IVRRLHSHVE	NMLDLAWERG	FVSQYECDEI	RLPIFTPSQR
240	ARRLLDLATV	KANGLAAFLI	QHVQELPVPL	ALPLEAATCK	KYMAKLRTTV	SAQSRFLSTY
300	DGAETLCLED	IYTENVLEW	ADVGMAGSPQ	KSPATLGLEE	LFSTPGHLND	DADTVLVVGE
360	AGSGKSTLLQ	RLHLLWAAGQ	DFQEFLFVFP	FSCRQLQCMA	KPLSVRTLIF	EHCCWPDVGQ
420	EDIFQLLLDH	PDRVLLTFDG	FDEFKFRFTD	RERHCSPTDP	TSVQTLLFNL	LQGNLLKNAR
480	KVVTSRPAAV	SAFLRKYIRT	EFNLKGFSEQ	GIELYLKRKH	HEPGVADRLI	RLQETSALH
540	GLCHLPVFSW	MVSKCHQELL	LQEGGSPKTT	TDMYLLILQH	FLLHATPPDS	ASQGLGPSLL
600	RGRPLPTLLHL	GRLALWGLGM	CCYVFSAQQL	QAAQVSPDDI	SLGFLVRAGV	VVPGSTAPLE
660	FLHITFQCFF	AAFYLALSAD	VPPALLRHLF	NCGRPGNSPM	ARLLPTMCIQ	ASEGKDSSVA
720	ALLQKAEPHN	LQITAAFLAG	LLSREHWGLL	AECQTSEKAL	LRRQACARWC	LARSLRKHFH
780	SIPPAAPGEA	KSVHAMPGFI	WLIRSLYEMQ	EERLARKAAR	GLNVGHLKLT	FCSVGPTeca
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960	LQFLGFWGNR	VGDEGAQALA	EALGDHQSIR	WLSLVGNNIG	SVGAQALALM	LAKNVMLEEL
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Figure 23
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Figure 24
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10002574.10260.1

Figure 25
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tga

10002574.102604

SNP	Allele	SNP Sequence*	AA Polymorphism	AA Location	cDNA Location
SNP4	1	GGCAGATGTGGGCATGGCTGGACCC; SEQ ID NO:70	P	P 268 S	nt 802
	2	GGCAGATGTGGGCATGGCTGGAICC; SEQ ID NO:71	S		
SNP20	1	AGACATCTGAGAAGGCCCTGCTCCGG; SEQ ID NO:72	R	R 702 W	nt 2104
	2	AGACATCTGAGAAGGCCCTGCTCTGG; Seq ID NO:73	W		
SNP7	1	CTGCAGCACCTCCGGCGGCCCGT; SEQ ID NO:74	V	V 793 M	nt 2377
	2	CTGCAGCACCTCCGGCGGCCCATG; SEQ ID NO:75	M		
SNP18	1	TTGCAGAAGTTAGCTCTATTCAAC; SEQ ID NO:76	N	N 852 S	nt 2555
	2	TTGCAGAAGTTAGCTCTATTGAGC; SEQ ID NO:77	S		
SNP25	1	ACTGACGGCTGTGCACACTCCATG; SEQ ID NO:78	M	M 863 V	nt 2587
	2	ACTGACGGCTGTGCACACTCCGTG; SEQ ID NO:79	V		
SNP17	1	TGCAGTTCCTGGGATTCTGGGGC; SEQ ID NO:80	G	G 908 R	nt 2722
	2	TGCAGTTCCTGGGATTCTGGCGC; SEQ ID NO:81	R		
SNP23	1	CACTGATGCTGGCAAAGAACGTC; SEQ ID NO:82	V	V 955 I	nt 2863
	2	CACTGATGCTGGCAAAGAACATC; SEQ ID NO:83	I		
3020C Ins	1	GGGCAGAAAGCCCTCCTGCAGGCCCT; SEQ ID NO:90	wild-type		nt 3020
	2	GGGCAGAAAGCCCTCCTGCAGGCCCT; SEQ ID NO:91	frameshift mutation	Δ33	
		*Underlined is mutated base			
		*Nucleotide/amino acid numbers designate the positions in Nod2a as reported by Ogura et al. J. Biol. Chem. 276:4812 [2001]			
		AA = amino acid			
		SNP= single nucleotide polymorphism			

Figure 26

Figure 28
SEQ ID NO: 59

MGEEGGSASHDEEERASVLLGHSPGCEMCSQEAFQAQRSQVLELLVSGSLEGFESVLDWLLSWEVLSWEDYEGFHLGQP
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FVSQYECDEIRLPIFTPSQRARRLLDLATVKANGLAAFLQHVQELPVPLALPLEAATCKKYMALRTTVSAQSRFLSTY
DGAETLCLEDIYTENVLEVWADVGMAGPPQKSPATLGLEELFSTPGHLNDDADTVLVVGEAGSGKSTLLQRLHLLWAAGQ
DFQEFLLFVFPFSCRQLQCMAPLSVRTLLFEHCCWPDVGQEDIFQLLLDHPDRVLLTFDGFDEFKFRFTDRERHCSPTDP
TSVQTLLFNLLQGNLLKNARKVVTSRPAAVSAFLRKYIRTEFNLKGFSEQGIELYLRKRHHEPGVADRLIRLLQETSALH
GLCHLPVFSWMVSKCHQELLLQEGGSPKTTTDMYLLILQHFLHATPPDSASQGLGPSLLRGRLLPTLLHLGRLLALWGLGM
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ARLLPTMCIQASEGKDSSVAALLQKAEPHNLQITAAFLAGLLSREHWGLLAECQTSEKALLRRQACARWCLARSLRKHFH
SIPPAAPGEAKSVHAMPGFIWLIRSLYEMQEERLARKAARGLNVGHLKLTFCSVGPTCAALAFVLQHLRRPVALQLDYN
SVGDIGVEQLLPCLGVCKALYLRDNNISDRGICKLIECALHCEQLQKLALFNNKLTGCAHSMAKLLACRQNFALRLGN
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*

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Figure 29
SEQ ID NO: 60

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tga

10002974.102601

Figure 30
SEQ ID NO: 61

MGEEGGSASHDEEERASVLLGHSPGCEMCSQEAFQAQRSQVLVSGSLEGFESVLDWLLSWEVLSWEDYEGFHLLGQP
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FVSQYECDEIRLPIFTSPQRARRLLDLATVKANGLAAFLQHVQELPVPLALPLEAATCKKYMALRTTVSAQSRFLSTY
DGAETLCLEDIYTENVLEVWADVGMAGSPQKSPATLGLEELFSTPGHLNDDADTVLVVGEAGSGKSTLLQRLHLLWAAGQ
DFQEFLFVFPFSCRQLQCMAPLSVRTLLFEHCCWPDVGQEDIFQLLLDHPDRVLLTFDGFDEFKFRFTDRERHCSPTDP
TSVQTLLFNLLQGNLLKNARKVVTSRPAAVSAFLRKYIRTEFNLKGFSEQGIELYLRKRHHEPGVADRLIRLLQETSALH
GLCHLPVFSWMVSKCHQELLQEGGSPKTTTDMYLLILQHFLHATPPDSASQGLGPSLLRGRPLTLLHLGRLLALWGLGM
CCYVFSQQQLQAAQVSPDDISLGFLVRAKGVVPGSTAPLEFLHITFQCFFAIFYLALSADVPPALLRHLFNCGRPGNSPM
ARLLPTMCIQASEGKDSSVAALLQKAEPHNLQITAAFLAGLLSREHWGLLAECQTSEKALLRRQACARWCLARSLRKHFH
SIPPAAPGEAKSVHAMPGFIVLIRSLYEMQEERLARKAARGLNVGHLKLTFCVGPTECAALAFVLQHLRRPVALQLDYN
SVGDIGVEQLLPCLGVCKALYLRDNNISDRGICKLIECALHCEQLQKLALFNNKLTGCAHSMAKLLACRQNFALRLGN
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Figure 31
SEQ ID NO: 62

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tga

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Figure 32
SEQ ID NO: 63

MGEEGGSASHDEEERASVLLGHSPGCEMCSQEAFQAQRSQVLVELLVSGSLEGFESVLDWLLSWEVLSWEDYEGFHLLGQP
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FVSQYECDEIRLPIFTSPQRARRLLDLATVKANGLAAFLQHVQELPVPLALPLEAATCKKYMALRTTVSAQSRFLSTY
DGAETLCLEDIYTENVLEVWADVGMAGPPQKSPATLGLEELFSTPGHLNDDADTVLVVGEAGSGKSTLLQRLHLLWAAGQ
DFQEFLFVFPFSCRQLQCMAPLSVRTLLFEHCCWPDVGQEDIFQLLLDHPDRVLLTFDGFDEFKFRFTDRERHCSPTDP
TSVQTLLFNLLQGNLLKNARKVVTSRPAAVSAFLRKYIRTEFNLKGFSEQGIELYLRKRHHEPGVADRLIRLLQETSALH
GLCHLPVFSWMVSKCHQELLQEGGSPKTTTDMYLLILQHFLHATPPDSASQGLGPSLLRGRPLTLLHLGRLLALWGLGM
CCYVFSQAQQLQAAQVSPDDISLGFLVRAKGVVPGSTAPLEFLHITFQCFFAAYLALSADVPPALLRHLFNCGRPGNSPM
ARLLPTMCIQASEGKDSSVAALLQKAEPHNLQITAAFLAGLLSREHWGLLAECQTSEKALLRRQACARWCLARSLRKHFH
SIPPAAPGEAKSVHAMPGFIWLIRSLYEMQEERLARKAARGLNVGHLKLTFCSSVGPTCAALAFVLQHLRRPMALQLDYN
SVGDIGVEQLLPCLGVCKALYLRDNNISDRGICKLIECALHCEQLQKLALFNNKLTGCAHSMAKLLACRQNFALRLGN
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*

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Figure 33
SEQ ID NO: 64

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gccgcacaaccttcagatcacagcagccttctggcagggtgtgttcccgggagcactggggcctgctgggtgagtgcc
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tga

10002974.102601

Figure 34
SEQ ID NO: 65

MGEEGGSASHDEEERASVLLGHSPGCEMCSQEAFAQQRSQVLELLVSGSLEGFESVLDWLLSWEVLSWEDYEGFHLLGQP
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FVSQYECDEIRLPIFTPSQRARRLLDLATVKANGLAAFLQHVQELPVPLALPLEAATCKKYMALRTTVSAQSRFLSTY
DGAETLCLEDIYTENVLEVWADVGMAGPPQKSPATLGLEELFSTPGHLNDDADTVLVVGEAGSGKSTLLQRLHLLWAAGQ
DFQEFLFVFPFSCRQLQCMAPLSVRTLLFEHCCWPDVGQEDIFQLLLDHPDRVLLTFDGFDEFKFRFTDRERHCSPTDP
TSVQTLLFNLLQGNLLKNARKVVTSRPAAVSAFLRKYIRTEFNLKGFSEQGIELYLRKRHHEPGVADRLLIRLLQETSALH
GLCHLPVFSWMVSKCHQELLQEGGSPKTTTDMYLLILQHFLHATPPDSASQGLGPSLLRGRLPTLLHLGRLALWGLGM
CCYVFSQQQLQAAQVSPDDISLGFVRAKGVVPGSTAPLEFLHITFQCFFAAFYLALSADVPPALLRHLFNCGRPGNSPM
ARLLPTMCIQASEGKDSSVAALLQKAEPHNLQITAAFLAGLLSREHWGLLAECQTSEKALLRRQACARWCLARSLRKHFH
SIPPAAPGEAKSVHAMPGFIWLIRSLYEMQEERLARKAARGLVNGLKLTFCFSGPTECAALAFVLQHLRRPVVALQLDYN
SVGDIGVEQLLPCLGVCKALYLRDNNISDRGICKLIECALHCEQLQKLALFSNKLTDGCAHSMALLACRQNFALRLGN
NYITAAGAQVLAEGLRGNTSLQFLGFWGNRVGDEGAQALAEALGDHQSRLWLSLVGNNGSVGAQALALMLAKNVMLEEL
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*

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Figure 35
SEQ ID NO: 66

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tga

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Figure 36
SEQ ID NO: 67

MGEEGGSASHDEEERASVLLGHSPGCEMCSQEAFQAQRSQVVELLVSGSLEGFESVLDWLLSWEVLSWEDYEGFHLLGQP
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DGAETLCLEDIYTENVLEVWADVGMAGPPQKSPATLGLEELFSTPGHLNDDADTVLVVGEAGSGKSTLLQRLHLLWAAGQ
DFQEFLLFVFPFSCRQLQCMAPLSVRTLLFEHCCWPDVGQEDIFQLLLDHPDRVLLTFDGFDEFKFRFTDRERHCSPTDP
TSVQTLLFNLLQGNLLKNARKVVTSRPAAVSAFLRKYIRTEFNLKGFSEQGIELYLRKRHHEPGVADRILIRLLQETSALH
GLCHLPVFSWMVSKCHQELLQEGGSPKTTTDMYLLILQHFLHATPPDSASQGLGPSLLRGRLEPTLLHLGRLALWGLGM
CCYVFSAAQQLQAAQVSPDDISLGLFLVRAGVVPGSTAPLEFLHITFQCFFAAFYLAALSADVPPALLRHLFNCGRPGNSPM
ARLLPTMCIQASEGKDSSVAALLQKAEPHNLQITAAFLAGLLSREHWGLLAECQTSEKALLRRQACARWCLARSLRKHFH
SIPPAAPGEAKSVHAMPGFIWLIRSLYEMQEERLARKAARGLNVGHLKLTFCSSVGPTCAALAFVLQHLRRPVALQLDYN
SVGDIGVEQLLPCLGVCKALYLRDNNISDRGICKLIECALHCEQLQKLALFNNKLTGCAHSMKLLACRQNFALRLGN
NYITAAGAQVLAEGLRGNTSLQFLGFWGNRVGDEGAQALAEALGDHQSRLWLSLVGNNIGSVGAQALALMLAKNIMLEEL
CLEENHLQDEGVCSLAEGLKKNSSLKILKLSNNCITYLGAEALLQALERNDTILEVWLRGNTFSLEEVDKLGCRDTRLLL
*

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Figure 37
SEQ ID NO: 68

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tga

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Figure 38
SEQ ID NO: 69

MGEEGGSASHDEEERASVLLGHSPGCEMCSQEAFQAQRSQVLELLVSGSLEGFESVLDWLLSWEVLSWEDYEGFHLLGQP
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FVSQYECDEIRLPIFTPSQRARRLLDLATVKANGLAAFLQHVQELPVPLALPLEAATCKKYMALRTTVSAQSRFLSTY
DGAETLCLEDIYTENVLEVWADVGMAGPPQKSPATLGLEELFSTPGHLNDDADTVLVVGEAGSGKSTLLQRLHLLWAAGQ
DFQEFLFVFPFSCRQLQCMAPLSVRTLLFEHCCWPDVGQEDIFQLLLDHPDRVLLTFDGFDEFKFRFTDRERHCSPTDP
TSVQTLLFNLLQGNLLKNARKVVTSRPAAVSAFLRKYIRTEFNLKGFSEQGIELYLRKRHHEPGVADRILIRLLQETSALH
GLCHLPVFSWMVSKCHQELLLQEGGSPKTTTDMYLLILQHFLHATPPDSASQGLGPSLLRGRPLTLLHLGRLLALWGLGM
CCYVFSAAQLQAAQVSPDDISLGFLVRAKGVVPGSTAPLEFLHITFQCFFAAFYLALSADVPPALLRHLFNCGRPGNSPM
ARLLPTMCIQASEGKDSSVAALLQKAEPHNLQITAAFLAGLLSREHWGLLAECQTSEKALLRRQACARWCLARSLRKHFH
SIPPAAPGEAKSVHAMPGFIWLIRSLYEMQEERLARKAARGNLVGHKLKTFCSVGPTCAALAFVLQHLRRPVALQLDYN
SVGDIGVEQLLPCLGVCKALYLRDNNISDRGICKLIECALHCEQLQKLALFNNKLTGCAHSVAKLLACRQNFALRLGN
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Figure 39
SEQ ID NO: 84

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tga

10002974-100001

Figure 40
SEQ ID NO: 85

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DGAETLCLEDIYTENVLEVWADVGMAGSPQKSPATLGLEELFSTPGHLNDDADTVLVVGEAGSGKSTLLQRLHLLWAAGQ
DFQEFLFVFPFSCRQLQCMAPLSVRTLLFEHCCWPDVGQEDIFQLLLDHPDRVLLTFDGFDEFKFRFTDRERHCSPTDP
TSVQTLLFNLLQGNLLKNARKVVTSRPAAVSAFLRKYIRTEFNLKGFSEQGIELYLRKRHHHEPGVADRILIRLLQETSALH
GLCHLPVFSWMVSKCHQELLQEGGSPKTTTDMYLLILQHFLHATPPDSASQGLGPSLLRGRLPDLLHLGRLLALWGLGM
CCYVFSQQQLQAAQVSPDDISLGFLVRAKGVVPGSTAPLEFLHITFQCFFAAFYLAALSADVPPALLRHLFNCGRPGNSPM
ARLLPTMCIQASEGKDSSVAALLQKAEPHNLQITAAFLAGLLSREHWGLLAECQTSEKALLRRQACARWCLARSLRKHFH
SIPPAAPGEAKSVHAMPGFIWLIRSLYEMQEERLARKAARGLNVGHLKLTFCVSGPTECAALAFVLQHLRRPVALQLDYN
SVGDIGVEQLLPCLGVCKALYLRDNNISDRGICKLIECALHCEQLQKLALFNNKLTGCAHSMAKLLACRQNFALRLGN
NYITAAGAVLAEGLRGNTSLQFLGFWRNRVGDEGAQALAEALGDHQSRLWLSLVGNNIGSVGAQALALMLAKNVMLEEL
CLEENHLQDEGVCSLAEGLLKNSSSLKILKLSNNCITYLGAEALLQALERNDTILEVWLRGNTFSLEEVDKLGCRDTRLLL
*

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Figure 41
SEQ ID NO: 86

atgggggaagaggggtgggttcagcctctcacgatgaggaggaaagagcaagtgtcctcctcggacattctccgggttgga
aatgtgctcgcaggaggcttttcaggcacagaggagccagctggctcgagctgctggctcagggccctggaaggcttcg
agagtgtcctggactggctgctgtcctgggaggtcctctcctgggaggactacgagggcttccacctcctgggcccagcct
ctctcccacttgggcaggcgcccttctggacaccgtctggaataaggggtacttgggctgtcagaagctcatcgcggtgc
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tgcagagtcacccggccagccattgtcaggaggctccacagccatgtggagaacatgtcggacctggcatgggagcgggt
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cctgaagttgtccaataactgcacacctacctaggggcagaagccctcctgcaggcccttgaaaggaatgacaccatcc
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tga

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Figure 42
SEQ ID NO: 87

MGEEGGSASHDEEERASVLLGHSPGCEMCSQEAFAQRSQVLELLVSGSLEGFESVLDWLLSWEVLSWEDYEGFHLLGQP
LSHLARRLLDTVWNKGTWACQKLIAAAQEAQADSQSPKLHGCWDPHSLHPARDLQSHRPAIVRRLHSHVENMLDLAWERG
FVSQYECDEIRLPIFTSPQRARRLLDLATVKANGLAAFLQHVQELPVPLALPLEAATCKKYMALRTTVSAQSRFLSTY
DGAETLCLEDIYTENVLEVWADVGMAGSPQKSPATLGLEELFSTPGHLNDDADTVLVVGEAGSGKSTLLQRLHLLWAAGQ
DFQEFLLFVFPFSCRQLQCMAPLSVRTLLFEHCCWPDVGQEDIFQLLLDHPDRVLLTFDGFDEFKFRFTDRERHCSPTDP
TSVQTLLENLLQGNLLKNARKVVTSRPAAVSAFLRKYIRTEFNLKGFSEQGIELYLRKRHHEPGVADRLLIRLLQETSALH
GLCHLPVFSWMVSKCHQELLLQEGGSPKTTTDMYLLILQHFLHATPPDSASQGLGPSLLRGRLPTLLHLGRLALWGLGM
CCYVFSQQQLQAAQVSPDDISLGFLVRAKGVVPGSTAPLEFLHITFCFFAAFYLAALSADVPPALLRHLFNCGRPGNSPM
ARLLPTMCIQASEGKDSSVAALLQKAEPHNLQITAAFLAGLLSREHWGLLAECQTSEKALLRRQACARWCLARSLRKHFH
SIPPAAPGEAKSVHAMPGFIWLIRSLYEMQEERLARKAARGLNVGHLKLTFCVSGPTECAALAFVLQHLRRPVALQLDYN
SVGDIGVEQLLPCLGVCKALYLRDNNISDRGICKLIECALHCEQLQKLALFSNKLTDGCAHSMALLACRQNFALRLGN
NYITAAGAQLAEGLRGNTSLQFLGFWGNRVGDEGAQALAEALGDHQSRLWLSLVGNNIGSVGAQALALMLAKNVMLEEL
CLEENHLQDEGVCSLAEGLKKNSSKILKLSNNCITYLGAEALLQALERNDTILEVWLRGNTFSLEEVDKLGCRDTRLLL
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Figure 43
SEQ ID NO: 88

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ccaagaagcccaggccgacagccagtcaccccaagctgcatggctgctgggacccccactcgctccaccagcccagagacc
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tga

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Figure 44
SEQ ID NO: 89

MGEEGGSASHDEEERASVLLGHSPGCEMCSQEAFAQRSQVLVSGSLEGFESVLDWLLSWEVLSWEDYEGFHLLGQP
LSHLARRLLDTVWNKGTWACQKLIAAAQEAQADSQSPKLHGCWDPHSLHPARDLQSHRPAIVRRLHSHVENMLDLAWERG
FVSQYECDEIRLPIFTSPQRARRLLDLATVKANGLAAFLQHVQELPVPLALPLEAATCKKYMALRTTVSAQSRFLSTY
DGAETLCLEDIYTENVLEVWADVGMAGSPQKSPATLGLEELFSTPGHLNDDADTVLVVGEAGSGKSTLLQRLHLLWAAGQ
DFQEFLFVFPFSCRQLQCMAPLSVRTLLFEHCCWPDVGQEDIFQLLLDHPDRVLLTFDGFDEFKFRFTDRERHCSPTDP
TSVQTLLFNLLQGNLLKNARKVVTSRPAAVSAFLRKYIRTEFNLKGFSEQGIELYLRKRHHEPGVADRLIRLLQETSALH
GLCHLPVFSWMVSKCHQELLQEGGSPKTTTDMYLLILQHFLHATPPDSASQGLGPSLLRGRLPTLLHLGRLALWGLGM
CCYVFSQQQLQAAQVSPDDISLGLVRAKGVVPGSTAPLEFLHITFQCFFAAFYLAALSADVPPALLRHLFNCGRPGNSPM
ARLLPTMCIQASEGKDSSVAALLQKAEPHNLQITAAFLAGLLSREHWGLLAECQTSEKALLWRQACARWCLARSLRKHFH
SIPPAAPGEAKSVHAMPGFIWLIRSLYEMQEERLARKAARGLNVGHLKLTFCVSGPTECAALAFVLQHLRRPVALQLDYN
SVGDIGVEQLLPCLGVCKALYLRDNNISDRGICKLIECALHCEQLQKLALFNNKLTGCAHSMALLACRQNFLALRLGN
NYITAAGAQVLAEGLRGNTSLQFLGFWGNRVGDEGAQALAEALGDHQSRLWLSLVGNNGSVGAQALALMLAKNVMLEEL
CLEENHLQDEGVCSLAEGLKKNSSLKILKLSNNCITYLGAEALLQALERNDTILEVWLRGNTFSLEEVDKLGCRDTRLLL
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